

REPLACEMENT SHEET

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Figure 1

M K H L W F F L L L V A A P R
GAC ATG AAA CAC CTG TGG TTC TTC CTC CTG GTG GCA GCC CCC AGA

+1
W V L S Q V Q L Q E A G P G L V
TGG GTC TTG TCC CAG GTG CAG CTG CAG GAG GCG GGC CCA GGA CTG GTG

20
K P S E T L S L T C S V S G G S
AAG CCT TCG GAG ACC CTG TCC CTC ACC TGC AGT GTC TCT GGT GGC TCC

30 40
I S G D Y Y W F W I R Q S P G K
ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA GGG AAG

50 60
G L E W I G Y I Y G S G G G T N
GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT

70
Y N P S L N N R V S I S I D T S
TAC AAT CCC TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC

80 90
K N L F S L K L R S V T A D T
AAG AAC CTC TTC TCC CTG AAA CTG AGG TCT GTG ACC GCC GCG GAC ACG

100
A V Y Y C A S N I L K Y L H W L
GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT CAC TGG TTA

110 120
L Y W G Q G V L V T V S S
TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA (SEQ ID NO:1)

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Figure 2

M A W A L L L L G L L A H F T
ACC ATG GCC TGG GCT CTG CTG CTC CTC GGC CTC CTT GCT CAC TTT ACA

+1 10
D S A A S Y E L S Q P R S V S V
GAC TCT GCG GCC TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG

20
S P G Q T A G F T C G G D N V G
TCC CCA GGA CAG ACG GCC GGG TTC ACC TGT GGG GGA GAC AAC GTT GGA

30 40
R K S V Q W Y Q Q K P P Q A P V
AGG AAA AGT GTA CAG TGG TAC CAG CAG AAG CCA CCG CAG GCC CCT GTG

50 60
L V I Y A D S E R P S G I P A R
CTG GTC ATC TAT GCT GAC AGC GAA CGG CCC TCA GGG ATC CCT GCG CGA

70
F S G S N S G N T A T L T I S G
TTC TCT GGC TCC AAC TCA GGG AAC ACC GCC ACC CTG ACC ATC AGC GGG

80 90
V E A G D E A D Y Y C Q V D S
GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGT

100
T A D H W V F G G G T R L T V L
ACT GCT GAT CAT TGG GTC TTC GGC GGA GGG ACC CGG CTG ACC GTC CTA

109
G
GGT (SEQ ID NO:3)

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Figure 3

Frame 1 Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp Ser Ala Ala
 ATG GCC TGG GCT CTG CTG CTG CTC GGC CTC CTT GCT CAC TTT TTT GGA CAG CCG GCG ACC
 9 18 27 36 45 54

Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser Pro Gly Gln Thr Ala Gly Phe Thr
 TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC CCA GGA CAG ACG GCC GGG TTC ACC
 66 75 84 93 102 111 120

Cys Gly Gly Asp Asn Val Gly Arg Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala
 TGT GGG GGA GAC AAC GTT GGA AGG AAA AGT GTA CAG TGG TAC GAG CAG AAG CCA CCG CAG GCC
 129 138 147 156 165 174 183

Pro Val Leu Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe Ser Gly
 CCT GTG CTG GTC ATC TAT GCT GAC AGC GAA GGG CCC TCA GGG ATC CCT GCG CGA TTC TCT GGC
 192 201 210 219 228 237 246

Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val Glu Ala Gly Asp Glu Ala Asp
 TCC AAC TCA GGG AAC ACC GGC ACC CTG ACC ATC AGC GGG GTC GAG GCC GGG GAT GAG GCT GAC
 255 264 273 282 291 300 309

Tyr Tyr Cys Gln Val Trp Asp Ser Thr Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu
 TAT TAC TGT CAG GTG TGG GAC AGT ACT GCT GAT CAT TGG GTC TTC GGC GGA GCC ACC CGG CTG
 318 327 336 345 354 363 372

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Thr Pro Pro Ser Ser Glu Glu
 ACC GTC CTA GGT CAG CCC AAG GCT GCC CCC TOG GTC ACT CTG TTC CCG CCC TCC TCT GAG GAG
 381 390 399 408 417 426 435

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr
 CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC TTC TAC CCG GGA GCC GTG ACA
 444 453 462 471 480 489 498

Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys
 GTG GCC TGG AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA
 507 516 525 534 543 552 561

Gln Ser Asn Asn Lys Tyr Ala Ala GCG GCC AGC Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
 CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG TGG AAG TCC
 570 579 588 597 606 615 624

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
 CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT
 633 642 651 660 669 678 687

Thr Glu Cys Ser THR
 ACA GAA TGT TCA TGA (SEQ ID NO:5)

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Figure 4

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser
 ATG AAA CAC CTG TGG TTC TTC CTC CTC GTG GCA GCC CCC AGA TGG GTC TTG TCC
 9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
 CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC
 66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro
 TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA
 129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro
 GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC
 192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu
 TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG AAG AAC CTC TTC TCC CTG AAA CTG
 255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu
 AGG TCT GTG ACC GCC GCG GAC ACG GCC CTC TAT TAC TGT GCG AGT AAT ATA ATG TAT CTT
 318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGC
 381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
 CCA TCC GTC TTT CCC GTC GCG CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC
 444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC
 507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG
 570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC
 633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro

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Figure 4 (Continued)

AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA TCA TGC CCA
696 705 714 723 732 741 750

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
GCA CCT GAG TTC CTG GGG GGA CCA TCA GTC TTC CCC CCA AAA CCC AAG GAC ACT CTC
759 768 777 786 795 804 813

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
ATG ATC TCC CGG ACC CCT GAG GTC ACG TGC GTG GTG GAC GTG AGC CAG GAA GAC CCC GAG
822 831 840 849 858 867 876

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
GTC CAG TTC AAC TGG TAC GTG GAT GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG
885 894 903 912 921 930 939

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
GAG CAG TTC AAC AGC ACG TAC CGT GTG GTC AGC CTC ACC GTC CTG CAC CAG GAC TGG CTG
948 957 966 975 984 993 1002

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
AAC GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC ATC CAG CAG ACC
1011 1020 1029 1038 1047 1056 1065

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
ATC TCC AAA GCC AAA GGG CAG CCC CGA GAG CCA CAG GTG TAC ACC CTG CCC CCA TCC CAG GAG
1074 1083 1092 1101 1110 1119 1128

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC
1137 1146 1155 1164 1173 1182 1191

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CAG
1200 1209 1218 1227 1236 1245 1254

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
GAC TCC GAC GGC TCC TTC CTC TAC TAC AGC AGG CTA ACC GTG GAC AAG AGC AGG TGG CAG GAG
1263 1272 1281 1290 1299 1308 1317

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
GGG AAT GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG AAG AGC
1326 1335 1344 1353 1362 1371 1380

Leu Ser Leu Ser Leu Gly Lys TER	
CTC TCC CTG TCT CTG GGT AAA TGA	(SEQ ID NO:7)
1389 1398	

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Figure 5

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser
 ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC
 9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
 CAG GTG CAG CTG CAG GAG GGC GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC
 66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro
 TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA
 129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro
 GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC
 192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu
 TCC CTC AAC AAT GGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG
 255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu
 AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT
 318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG
 381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
 CCA TCC GTC TTC CCC CTG GCG GGC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC
 444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC
 507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG
 570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC
 633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro

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Figure 5 (Continued)

AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA TCA TGC CCA
696 705 714 723 732 741 750

Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
GCA CCT GAG TTC GAG GGG GGA CCA TCA GTC TTC CTG TTC CCC CCA AAA CCC AAG GAC ACT CTC
759 768 777 786 795 804 813

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
ATG ATC TCC CGG ACC CCT GAG GTC ACG TGC GTG GTG GTG GAC GTG AGC CAG GAA GAC CCC GAG
822 831 840 849 858 867 876

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
GTC CAG TTC AAC TGG TAC GTG GAT GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG
885 894 903 912 921 930 939

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
GAG CAG TTC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC GAG TGG CTG
948 957 966 975 984 993 1002

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
AAC GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC TCC ATC GAG AAA ACC
1011 1020 1029 1038 1047 1056 1065

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
ATC TCC AAA GCC AAA GGG CAG CCC CGA GAG CCA CAG GTG TAC ACC CTG CCC CCA TCC CAG GAG
1074 1083 1092 1101 1110 1119 1128

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC
1137 1146 1155 1164 1173 1182 1191

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
GCC GGC AAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG
1200 1209 1218 1227 1236 1245 1254

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
GAC TCC GAG GGC TCC TTC TTC TAC AGC AGG CTA ACC GTG GAC AAG AGC AGG TGG CAG GAG
1263 1272 1281 1290 1299 1308 1317

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
GGG AAT GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG AAG AGC
1326 1335 1344 1353 1362 1371 1380

Leu Ser Leu Ser Leu Gly Lys TER

CTC TCC CTG TCT CTG GGT AAA TGA (SEQ ID NO:9)
1389 1398

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Figure 6

Frame 1	Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	Val	Leu	Ser		
	ATG	AAA	CAC	CTG	TGG	TTC	TTC	CTC	CTC	CTG	GTG	GCA	GCC	CCC	AGA	TGG	GTC	TTG	CCC	
		9				18		27		36			45			54				
Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr
CAG	GTG	CAG	CTG	CAG	GAG	TGC	GGC	CCA	GGA	CTG	GTG	AAG	CGT	TCG	GAG	ACC	CTG	TCC	CTC	ACC
	66		75				84			93			102			111			120	
Cys	Ser	Val	Ser	Gly	Ser	Ile	Ser	Gly	Asp	Tyr	Tyr	Trp	Phe	Trp	Ile	Arg	Gln	Ser	Pro	
TGC	AGT	GTC	TCT	GGT	GGC	TCC	ATC	AGC	GGT	GAC	TAT	TAT	TGG	TTC	TGG	ATC	CGC	CAG	TCC	CCA
	129		138			147		156				165				174			183	
Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Gly	Ser	Gly	Gly	Gly	Thr	Asn	Tyr	Asn	Pro
GGG	AAG	GGA	CTG	GAG	TGG	ATC	GGC	TAC	ATC	TAT	GGC	AGT	GGT	GGG	GGC	ACC	AAT	TAC	AAT	CCC
	192		201			210		219				228				237			246	
Ser	Leu	Asn	Asn	Arg	Val	Ser	Ile	Ser	Ile	Asp	Thr	Ser	Lys	Asn	Leu	Phe	Ser	Leu	Lys	Leu
TCC	CTC	AAC	AAT	CGA	GTC	TCC	ATT	TCA	ATA	GAC	ACG	TCC	AAG	AAC	CTC	TTC	TCC	CTG	AAA	CTG
	255		264			273		282				291				300			309	
Arg	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ser	Asn	Ile	Leu	Lys	Tyr	Leu
AGG	TCT	GTG	ACC	GCC	GCG	GAC	ACG	GCC	GTC	TAT	TAC	TGT	GCG	AGT	AAT	ATA	TTG	AAA	TAT	CTT
	318		327			336		345				354				363			372	
His	Trp	Leu	Leu	Tyr	Trp	Gly	Gln	Gly	Val	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
CAC	TGG	TTA	TTA	TAC	TGG	GGC	CAG	GGA	GTC	CTG	GTC	ACC	GTC	TCC	TCA	GCT	AGC	ACC	AAG	GGG
	381		390			399		408				417				426			435	
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly
CCA	TCC	GTG	TTC	CCC	CTG	GCG	CCC	TGC	TCC	AGG	AGC	ACC	TCC	GAG	AGC	ACA	GCC	GCC	CTG	GGC
	444		453			462		471				480				489			498	
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA	GAC	GCC	CTG	ACC
	507		516			525		534				543				552			561	
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val
AGC	GGC	GTG	CAC	ACC	TTC	CGC	GCT	GTC	CTA	CAG	TCC	CTC	GGA	CTC	TAC	TCC	CTC	AGC	AGC	GTG
	570		579			588		597				606				615			624	
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro
GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACG	AAG	ACC	TAC	ACC	TGC	AAC	GTA	GAT	CAC	AAG	CCC
	633		642			651		660				669				678			687	
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro

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Figure 6 (Continued)

AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA CCA TGC CCA
596 705 714 723 732 741 750

Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
GCA CCT GAG TTC GAG GGG GGA CCA TCA GTC TTC CTG TTC CCC CCA AAA CCC AAG GAC ACT CTC
759 768 777 786 795 804 813

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
ATG ATC TCC CGG ACC CCT GAG GTC ACG TGC GTG GTG GAC GTG AGC CAG GAA GAC CCC GAG
822 831 840 849 858 867 876

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
GTC CAG TTC AAC TGG TAC GAT GAT GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CCG GAG
885 894 903 912 921 930 939

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
GAG CAG TTC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC GAC TGG CTG
948 957 966 975 984 993 1002

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
AAC GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC TCC ATC GAC AAA ACC
1011 1020 1029 1038 1047 1056 1065

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
ATC TCC AAA GCC AAA GGG CAG CCC CGA GAG CCA CAG GTG TAC ACC CTG CCC CCA TCC CAG GAG
1074 1083 1092 1101 1110 1119 1128

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC
1137 1146 1155 1164 1173 1182 1191

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACC CCA CCG CCG GTG
1200 1209 1218 1227 1236 1245 1254

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
GAC TCC GAC GGC TCC TTC CTC TAC AGC AGG CTA ACC GTG GAC AAG AGC AGG TGG CAG GAG
1263 1272 1281 1290 1299 1308 1317

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
GGG AAT GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG AAG AGC
1326 1335 1344 1353 1362 1371 1380

Leu Ser Leu Ser Leu Gly Lys TER
CTC TCC CTG TCT CTG GGT AAA TGA (SEQ ID NO:11)
1389 1398

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Figure 7-1

Primers for the Amplification of Monkey Immunoglobulin Heavy Chain Variable Regions5' 'Sense' PrimersA. Human or Monkey heavy chain early leader sequence primers with *Sal*I site

V _H 1	5' ACTAAGTCGACATGGACTGGACCTTGG 3'	(SEQ ID NO:13)
V _H 2	5' ACTAAGTCGACATGGACATACTTTGTTCCAC 3'	(SEQ ID NO:14)
V _H 3	5' ACTAAGTCGACATGGAGTTTGGGCTGAGC 3'	(SEQ ID NO:15)
V _H 4	5' ACTAAGTCGACATGAAACACCTGTGGTCTT 3'	(SEQ ID NO:16)
V _H 5	5' ACTAAGTCGACATGGGGTCAACGCCATCCT 3'	(SEQ ID NO:17)
V _H 6	5' ACTAAGTCGACATGTCTGTCTCCTTCCTCAT 3'	(SEQ ID NO:18)

B. Human or Monkey heavy chain late leader sequence primers with *Mlu*I site

V _H 1	5' G GCA GCA GC (CT) <u>ACG CGT</u> GCC CAC TCC GAG GT 3'	(SEQ ID NO:19)
V _H 2	5' G ACC GTC CCG <u>ACG CGT</u> GT (TC) TTG TCC CAG GT 3'	(SEQ ID NO:20)
V _H 3	5' GCT ATT TTC <u>ACG CGT</u> GTC CAG TGT GAG 3'	(SEQ ID NO:21)
V _H 4	5' GCG GCT CCC <u>ACG CGT</u> GTC CTG TCC CAG 3'	(SEQ ID NO:22)
V _H 5	5' G GCT GTT CTC <u>ACG CGT</u> GTC TGT GCC GAG GT 3'	(SEQ ID NO:23)

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Figure 7-1 (Continued)

C. Human or Monkey framework 1 sequence primers with Xho / site

V _H 1,3a,5	+1 CAGGTGCAGCTGCTCGAGTCTGG	(SEQ ID NO:24)
V _H 2	+1 CAGGTCAACTTACTCGAGTCTGG	(SEQ ID NO:25)
V _H 3b	+1 GAGGTGCAGCTGCTCGAGTCTGG	(SEQ ID NO:26)
V _H 4	+1 CAGGTGCAGCTGCTCGAGTCGGG	(SEQ ID NO:27)
V _H 6	+1 CAGGTACAGCTGCTCGAGTCAGG	(SEQ ID NO:28)

3' 'Anti-Sense' PrimersA. Human or Monkey heavy chain constant region primers anti-sense strand with Nhe 1 site

IgG ₁₋₄	+118 5' GGC GGA TGC GCT AGC TGA GGA GAC GG 3'	(SEQ ID NO:29)
	Nhe 1	

Figure 7-2

Primers for the Amplification of Monkey Immunoglobulin Light Chain Variable Regions

5' Sense' Primers

A. Human or Monkey kappa light chain early leader primers with Bgl II site

1. 5' ATCACAGATCTCTCACCATGGTGTGGCAGACCCAGGTC 3' (SEQ ID NO:30)
2. 5' ATCACAGATCTCTCACCATGG (GA) G (AT) CCCC (TA) GC (TG) CAGCT 3' (SEQ ID NO:31)
3. 5' ATCACAGATCTCTCACCATGGACATGAGGGTCCCGCTCAG 3' (SEQ ID NO:32)
4. 5' ATCACAGATCTCTCACCATGGACAC (GAC) AGGGCCCCCACTCAG 3' (SEQ ID NO:33)

B. Human or Monkey lambda light chain early leader primers with Bgl II site

1. 5' ATCACAGATCTCTCACCATGGCCTGGGCTCTGCTGTCTCC 3' (SEQ ID NO:34)
2. 5' ATCACAGATCTCTCACCATGGCCTGGGCTCCACTACTTC 3' (SEQ ID NO:35)
3. 5' ATCACAGATCTCTCACCATGACCTGCTCCCTCTCTCTCC 3' (SEQ ID NO:36)
4. 5' ATCACAGATCTCTCACCATGGCCTGGACTCTCTCTTTTC 3' (SEQ ID NO:37)
5. 5' ATCACAGATCTCTCACCATGACTTGGACCCCCACTCTCTC 3' (SEQ ID NO:38)

3' 'Anti-Sense' Primers

A. Human or Monkey kappa light chain constant region primer anti-sense strand with *Kpn* 1 and *Bsi*W1 sites

C-Kappa

	+108		+97
5'	CCG TTT GAT TTC CAG CTT GGT ACC TCC ACC GAA CGT 3'		

(SEQ ID NO:39)

5' TGC AGC ATC CGT ACG TTT GAT TTC CAG CTT 3' +103
+112 BstW1 (SEQ ID NO:40)

B. Human or Monkey lambda light chain constant region primer anti-sense strand with

Kpn 1, Hind III and Avr II sites

C_{Lambda}

5' ACC TAG GAC GGT AAG CTT GGT ACC TCC GCC 3'

+107 +99

(SEQ ID NO:41)

5' ACC TAG GAC GGT CA (C/G) (C/G) TT GGT ACC TCC GCC GAA CAC 3' (SEQ ID NO:42)

5' CTT⁺¹¹⁰ GGG CTG ACC TAG GAC GGT GAG CCG 3'⁺¹⁰²
Avr II

Figure 8

A. Heavy chain variable region:

VH1	5' CCATGGACTGGACCTGG 3'	(SEQ ID NO:44)
VH2	5' ATGGACATACTTTTGTTCAC 3'	(SEQ ID NO:45)
VH3	5' CCATGGAGTTGGGCTGAGC 3'	(SEQ ID NO:46)
VH4	5' ATGAAACACCTGTGGTTCTT 3'	(SEQ ID NO:47)
VH5	5' ATGGGTCACCGCCATCCT 3'	(SEQ ID NO:48)
VH6	5' ATGTCTGTCTCTTCCTCAT 3'	(SEQ ID NO:49)

B. Heavy chain constant region anti-sense strand:

IgM	5' T TGG GGC GGA TGC ACT 3'	(SEQ ID NO:50)
IgG ₁₋₄	5' GA TGG GCC CTT GGT GGA 3'	(SEQ ID NO:51)

C. Light chain variable region:

Kappa	5' G ATG ACC CAG TCT CCA (G/T) CC TC 3'	(SEQ ID NO:52)
Lambda	5' CTC A (C/T) T (T/C) (G/A) C TGC (A/C) CA GGG TCC 3'	(SEQ ID NO:53)

D. Light chain constant region anti-sense strands:

Kappa	5' AA GAC AGA TGG TGC AGC CA 3'	(SEQ ID NO:54)
Lambda	5' G GAA CAG AGT GAC CGA GGG G 3'	(SEQ ID NO:55)

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Figure 16

PCR Primers for Human $\gamma 4$ Constant Region

1) IDEC 462 3' PCR Primer
 5' GGGG GGA TCC TCA TTT ACC CAG AGA CAG GG 3'
 BamH I (SEQ ID NO:56)

2) IDEC 479 5' PCR Primer
 5' GGGG GCT AGC ACC AAG GGC CCA TCC GTC TTC 3'
 Nhe I (SEQ ID NO:57)

PCR Mutagenesis of Human $\gamma 4$

3) IDEC 698 3' PCR Primer
 5' CCG GGA GAT CAT GAG AGT GTC CTT GGG TTT TGG GGG GAA CAG GAA GAC
 BspH I
 TGA TGG TCC CCC CTC GAA CTC AGG TGC TGG GCA TGG TGG GCA TGG GGG 3'
 Glu Pro (SEQ ID NO:58)

4) Midland GE212 5' PCR Primer
 Nhe I
 5' TCC TCA GCT AGC ACC AAG GGG CCA TCC 3'
 Destroys Apa I site (SEQ ID NO:59)

REPLACEMENT SHEET

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Figure 17

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser
 ATG AAA CAC CTG TGG TTC TTC CTC CTC GCA GCC CCC AGA TGG GTC TTG CCC
 9 18 27 36 45 54

+1
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
 CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC
 66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro
 TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA
 129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro
 GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC
 192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu
 TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG
 255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu
 AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT
 318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG
 381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
 CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC
 444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC
 507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA GAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG
 570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Cys Asn Val Asp His Lys Pro
 GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC
 633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro

REPLACEMENT SHEET

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Figure 17 (Continued)

AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA CCA TGC CCA
696 705 714 723 732 741 750

Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
GCA CCT GAG TTC GAG GGG GGA CCA TCA GTC TTC CTG TTC CCC CCA AAA CCC AAG GAC ACT CTC
759 768 777 786 795 804 813

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
ATG ATC TCC CGG ACC CCT GAG GTC ACG TGC GTG GTG GAC GTG AGC CAG GAA GAC CCC GAG
822 831 840 849 858 867 876

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
GTC CAG TTC AAC TGG TAC GAT GGT GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG
885 894 903 912 921 930 939

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
GAG CAG TTC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG
948 957 966 975 984 993 1002

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
AAC GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC TCC ATC GAG AAA ACC
1011 1020 1029 1038 1047 1056 1065

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
ATC TCC AAA GCC AAA GGG CAG CCC CGA GAG CCA CAG GTG TAC ACC CTG CCC CCA TCC CAG GAG
1074 1083 1092 1101 1110 1119 1128

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC
1137 1146 1155 1164 1173 1182 1191

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAT TAC AAG ACC ACG CCT CCC CTG CTG
1200 1209 1218 1227 1236 1245 1254

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
GAC TCC GAC GGC TCC TTC CTC TAC AGC AGG CTA ACC GTG GAC AAG AGC AGG TGG CAG GAG
1263 1272 1281 1290 1299 1308 1317

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
GGG AAT GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAG CAC TAC ACA CAG AAG AGC
1326 1335 1344 1353 1362 1371 1380

Leu Ser Leu Ser Leu Gly Lys TER
CTC TCC CTG TCT CTG GGT AAA TGA (SEQ ID NO:11)
1389 1398